WHAT IS CLAIMED IS:

1. An antisense oligonucleotide comprising at least one non-naturally occurring backbone linkage and between 6 and about 50 bases, wherein at least one of said bases are universal and/or degenerate bases and, wherein said antisense oligonucleotide complements at least two RNA molecules of a different sequence.

2. The antisense oligonucleotide of Claim 1, wherein no more than about 50% of said bases are universal and/or degenerate bases.

3. An antisense oligonucleotide comprising a first non-RNase H recruiting region of between 3 and about 15 bases, an RNase H recruiting region of between 3 and about 15 bases, and a second non-RNase H recruiting region, wherein at least one of said bases are universal and/or degenerate bases and, wherein said antisense oligonucleotide complements at least two RNA molecules of a different sequence.

4. The antisense oligonucleotide of Claim 3, wherein no more than about 50% of said bases are universal and/or degenerate bases.

5. An antisense oligonucleotide comprising a non-RNase H recruiting section and an RNase H recruiting section, wherein at least one of said bases are universal and/or degenerate bases and, wherein said antisense oligonucleotide complements at least two RNA molecules of a different sequence.

6. The antisense oligonucleotide of Claim 5, wherein no more than about 50% of said bases are universal and/or degenerate bases.

7. An antisense oligonucleotide comprising an RNase L-recruiting region comprising a 2'-5' adenosine oligomer, wherein an RNA targeting region of said antisense oligonucleotide comprises at least one universal and/or degenerate bases and, wherein said antisense oligonucleotide complements at least two RNA molecules of a different sequence.

8. The antisense oligonucleotide of Claim 7, wherein said RNA targeting region comprises no more than about 50% universal and/or degenerate bases.

9. An antisense oligonucleotide comprising an RNase P-recruiting region, wherein an RNA targeting region of said antisense oligonucleotide comprises at least one universal and/or degenerate bases and, wherein said antisense oligonucleotide complements at least two RNA molecules of a different sequence.

10. The antisense oligonucleotide of Claim 9, wherein said RNA targeting region comprises no more than about 50% universal and/or degenerate bases.

11. A ribozyme comprising an RNA targeting region, which comprises at least one universal and/or degenerate bases, wherein said antisense oligonucleotide complements at least two RNA molecules of a different sequence.

12. The ribozyme of Claim 11, wherein said RNA targeting region comprises no more than about 50% universal and/or degenerate bases.

13. A method of cleaving a plurality of target RNA molecules of different sequence, comprising contacting said target RNA molecules with an antisense oligonucleotide according to any one of Claims 1-10 in the presence of an RNAse capable of cleaving said target RNA molecules.

14. The method of Claim 13, wherein said RNase is selected from the group consisting of RNAse H, RNAse L, and RNAse P.

15. A method of cleaving a plurality of target RNA molecules of different sequence, comprising contacting said target RNA molecules with a ribozyme according to Claims 11 or 12.

16. A method of cleaving a plurality of target RNA molecules of different sequence, comprising contacting said target RNA molecules with an antisense oligonucleotide comprising between 6 and about 50 bases, wherein said antisense oligonucleotide comprises at least one universal and/or degenerate base and, wherein said antisense oligonucleotide complements at least two RNA molecules of a different sequence.

17. A method for reducing the deleterious effects of an antisense oligonucleotide comprising one or more sequence motifs, comprising replacing one or more bases within said one or more sequence motifs with one or more universal and/or degenerate bases.

18. The method of Claim 17, wherein said sequence motif is a CG dinucleotide.

19. The method of Claim 17, wherein said sequence motif is a poly-G sequence.